```
=> d his

        (FILE 'HOME' ENTERED AT 16:42:02 ON 15 SEP 2006)

        FILE 'MEDLINE, EMBASE, BIOSIS, SCISEARCH, DISSABS, TOXCENTER' ENTERED AT
        16:42:27 ON 15 SEP 2006
L1          173 S (KAPELLER-LIBERMANN R?/AU) OR (LIBERMANN R?/AU) OR (KAPELLER
L2            1 S L1 AND 47174
L3            1 S L1 AND GLYCOSYLTRANSFERASE
L4            0 S L1 AND (UDP-GALNAC? OR GALNAC? OR PPGALNAC?)
L5            0 S L1 AND (ACETYLGALACTOSAMINE? OR GALACTOSAMINE?)
L6            1 S L2 OR L3
L7            4 S GALNAC-T9 OR GALNACT9 OR UDP-GALNAC-T9 OR UDP-GALNACT9
L8            0 S PPGALNAC-T9 OR PPGALNACT9 OR UDP-PPGALNAC-T9 OR UDP-PPGALNACT
L9            1 S GALNAC? AND (TRANSFERASE (2A) 9)
L10           1 S GALNAC? AND (TRANSFERASE (2A) (9 OR T9 OR T-9))
L11           7 S GALNAC? AND (TRANSFERASE (5A) (9 OR T9 OR T-9))
L12          25 S GALNAC? AND (TRANSFERASE AND (T9 OR T-9))
L13          30 S L7 OR L9 OR L10 OR L11 OR L12
L14           9 DUP REM L13 (21 DUPLICATES REMOVED)
L15           1 DUP REM L7 (3 DUPLICATES REMOVED)
L16           7 S PPGANTASE-T9
L17           3 DUP REM L16 (4 DUPLICATES REMOVED)
L18           3 S PPGALNAC AND (T9 OR T-9 OR TRANSFERASE-9)
L19           3 S PPGALNAC? AND (T9 OR T-9 OR TRANSFERASE-9)
L20          15 S PPGANTASE? AND (T9 OR T-9 OR TRANSFERASE-9)
L21          18 S L19 OR L20
L22           6 DUP REM L21 (12 DUPLICATES REMOVED)

=> log y
```

PRINT OUT OF
SEQUENCE
SEARCH
RESULTS

3M
9/15/06

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OM protein - protein search, using sw model

Run on:        August 16, 2006, 00:37:10 ; Search time 195 Seconds
                                          (without alignments)
                                          1413.854 Million cell updates/sec

Title:         US-10-713-345-2
Perfect score: 3190
Sequence:      1 MAVARKIRTLLTVNILVFVG..........VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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               6:  geneseqp2003as:*
               7:  geneseqp2003bs:*
               8:  geneseqp2004s:*
               9:  geneseqp2005s:*
               10:  geneseqp2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                         SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	3190	100.0	603	6	ABG73283	Abg73283 Human 471
2	3190	100.0	603	7	ADC77653	Adc77653 Human 471
3	3190	100.0	603	8	ADM46166	Adm46166 Human 471
4	2052.5	64.3	598	5	ABG32380	Abg32380 Novel hum
5	2052.5	64.3	598	5	ABP53502	Abp53502 Human pp-
6	2047.5	64.2	598	7	ADC35390	Adc35390 Human N-a
7	2044.5	64.1	598	8	ADS10894	Ads10894 Human the
8	2037	63.9	402	4	AAM40398	Aam40398 Human pol
9	1996.5	62.6	560	4	AAM41675	Aam41675 Human pol
10	1732	54.3	468	7	ADE47680	Ade47680 Human NOV
11	1732	54.3	468	8	ADJ78950	Adj78950 Human NOV
12	1732	54.3	468	8	ADJ71667	Adj71667 Human NOV
13	1732	54.3	468	8	ADJ71669	Adj71669 Human NOV
14	1732	54.3	468	8	ADJ71661	Adj71661 Human NOV
15	1731	54.3	468	8	ADJ71665	Adj71665 Human NOV
16	1727	54.1	315	4	AAM42184	Aam42184 Human pol
17	1625	50.9	435	8	ADJ71663	Adj71663 Human NOV
18	1586	49.7	607	5	AAE22155	Aae22155 Human TRN
19	1586	49.7	607	6	ADA54308	Ada54308 Human pro
20	1586	49.7	607	7	ADC35389	Adc35389 Human N-a
21	1571	49.2	607	7	ADE47686	Ade47686 Human NOV
22	1571	49.2	607	7	ADE47688	Ade47688 Human NOV
23	1571	49.2	607	7	ADE47690	Ade47690 Human NOV
24	1571	49.2	607	8	ADJ78958	Adj78958 Human NOV
25	1571	49.2	607	8	ADJ78956	Adj78956 Human NOV
26	1571	49.2	607	8	ADJ78960	Adj78960 Human NOV
27	1478	46.3	407	4	ABB15037	Abb15037 Human ner
28	1474	46.2	354	6	ADA54187	Ada54187 Human pro
29	1431	44.9	266	3	AAB41739	Aab41739 Human ORF
30	1118	35.0	358	4	AAM40865	Aam40865 Human pol
31	1118	35.0	358	8	ADS12137	Ads12137 Human the
32	1085	34.0	297	7	ADB64287	Adb64287 Human pro
33	1085	34.0	297	8	ADQ66754	Adq66754 Novel hum
34	1077	33.8	297	7	ADM04203	Adm04203 Human pro
35	1077	33.8	297	9	AEC87133	Aec87133 Human cDN
36	1076	33.7	297	4	AAM39079	Aam39079 Human pol
37	949	29.7	177	7	ADE25972	Ade25972 N-acetylg
38	949	29.7	177	9	ADX58133	Adx58133 Human pol
39	949	29.7	177	9	ADX58235	Adx58235 Human pol
40	939	29.4	571	7	ADC10116	Adc10116 Human NOV
41	931.5	29.2	556	5	ABG32379	Abg32379 Novel hum
42	931.5	29.2	556	7	ADE25918	Ade25918 Novel N-a

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:47:04 ; Search time 51 Seconds
                                             (without alignments)
                                             1034.921 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLLTVNILVFVG.........VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result   Query
  No.   Score   Match Length DB ID   Description
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    2   1586   49.7   607   2 US-10-094-749-1876   Sequence 1876, Ap
    3   1474   46.2   354   2 US-10-094-749-1755   Sequence 1755, Ap
    4   1085   34.0   297   2 US-10-104-047-2441   Sequence 2441, Ap
    5   906.5   28.4   517   1 US-08-967-508-19   Sequence 19, Appl
    6   906.5   28.4   517   2 US-08-967-506-19   Sequence 19, Appl
    7   906.5   28.4   517   5 PCT-US94-02552-19   Sequence 19, Appl
    8   906.5   28.4   559   1 US-08-967-508-9   Sequence 9, Appli
    9   906.5   28.4   559   2 US-08-967-506-9   Sequence 9, Appli
   10   906.5   28.4   559   5 PCT-US94-02552-9   Sequence 9, Appli
   11   844   26.5   578   2 US-10-074-527-8   Sequence 8, Appli
   12   836   26.2   578   2 US-09-217-306B-2   Sequence 2, Appli
   13   833   26.1   560   2 US-09-217-306B-10   Sequence 10, Appl
   14   782.5   24.5   581   2 US-10-074-527-2   Sequence 2, Appli
   15   761   23.9   552   2 US-10-104-047-2405   Sequence 2405, Ap
   16   757   23.7   633   1 US-08-648-298-2   Sequence 2, Appli
   17   744   23.3   603   2 US-09-795-926-43   Sequence 43, Appl
   18   744   23.3   603   2 US-10-364-774-43   Sequence 43, Appl
   19   731   22.9   506   2 US-09-795-926-31   Sequence 31, Appl
   20   731   22.9   506   2 US-10-364-774-31   Sequence 31, Appl
   21   722.5   22.6   631   2 US-09-795-926-41   Sequence 41, Appl
   22   722.5   22.6   631   2 US-10-364-774-41   Sequence 41, Appl
   23   709.5   22.2   535   2 US-09-795-926-29   Sequence 29, Appl
   24   709.5   22.2   535   2 US-10-364-774-29   Sequence 29, Appl
   25   694   21.8   639   2 US-09-376-856-2   Sequence 2, Appli
   26   694   21.8   639   2 US-10-012-231A-347   Sequence 347, App
   27   694   21.8   639   2 US-10-015-389A-347   Sequence 347, App
   28   694   21.8   639   2 US-10-006-768A-347   Sequence 347, App
   29   694   21.8   639   2 US-10-015-671A-347   Sequence 347, App
   30   694   21.8   639   2 US-10-015-393A-347   Sequence 347, App
   31   694   21.8   639   2 US-10-011-833A-347   Sequence 347, App
   32   694   21.8   639   2 US-10-006-041A-347   Sequence 347, App
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   37   694   21.8   639   3 US-10-012-121A-347   Sequence 347, App
   38   694   21.8   639   3 US-10-006-485A-347   Sequence 347, App
   39   694   21.8   639   3 US-10-006-746A-347   Sequence 347, App
   40   694   21.8   639   3 US-10-012-752A-347   Sequence 347, App
   41   694   21.8   639   3 US-10-017-253A-347   Sequence 347, App
   42   694   21.8   639   3 US-10-015-519A-347   Sequence 347, App
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   44   694   21.8   639   3 US-10-007-236A-347   Sequence 347, App
   45   688   21.6   638   2 US-09-347-488-2   Sequence 2, Appli

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OM protein - protein search, using sw model

Run on:          August 16, 2006, 00:51:25 ; Search time 183 Seconds
                                            (without alignments)
                                            1526.331 Million cell updates/sec

Title:           US-10-713-345-2
Perfect score:   3190
Sequence:        1 MAVARKIRTLLTVNILVFVG.........VQRCSGQKWMIRNWIKHARH 603

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:     2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_Main:*
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                 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                          SUMMARIES
                 %
                 Query
Result
No.     Score  Match Length DB  ID                     Description
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    2   3190   100.0   603   4   US-10-369-022-16       Sequence 16, Appl
    3   3190   100.0   603   4   US-10-184-648-43       Sequence 43, Appl
    4   3190   100.0   603   4   US-10-713-345-2        Sequence 2, Appli
    5   2052.5  64.3   598   4   US-10-060-895A-3       Sequence 3, Appli
    6   2052.5  64.3   598   5   US-10-467-903-10       Sequence 10, Appl
    7   1732    54.3   468   4   US-10-210-130-42       Sequence 42, Appl
    8   1732    54.3   468   5   US-10-635-398-62       Sequence 62, Appl
    9   1732    54.3   468   5   US-10-635-398-68       Sequence 68, Appl
   10   1732    54.3   468   5   US-10-635-398-70       Sequence 70, Appl
   11   1731    54.3   468   5   US-10-635-398-66       Sequence 66, Appl
   12   1625    50.9   435   5   US-10-635-398-64       Sequence 64, Appl
   13   1586    49.7   607   4   US-10-288-252-17       Sequence 17, Appl
   14   1586    49.7   607   4   US-10-094-749-1876     Sequence 1876, Ap
   15   1586    49.7   607   4   US-10-398-038-17       Sequence 17, Appl
   16   1586    49.7   607   5   US-10-976-440-17       Sequence 17, Appl
   17   1571    49.2   607   4   US-10-210-130-48       Sequence 48, Appl
   18   1571    49.2   607   4   US-10-210-130-50       Sequence 50, Appl
   19   1571    49.2   607   4   US-10-210-130-52       Sequence 52, Appl
   20   1474    46.2   354   4   US-10-094-749-1755     Sequence 1755, Ap
   21   1085    34.0   297   4   US-10-104-047-2441     Sequence 2441, Ap
   22   1085    34.0   297   6   US-11-072-512-2441     Sequence 2441, Ap
   23   1077    33.8   297   4   US-10-108-260A-2888    Sequence 2888, Ap
   24   949     29.7   177   4   US-10-292-896-116      Sequence 116, App
   25   949     29.7   177   5   US-10-705-401-11       Sequence 11, Appl
   26   949     29.7   177   5   US-10-705-401-113      Sequence 113, App
   27   931.5   29.2   556   4   US-10-292-896-62       Sequence 62, Appl
   28   931.5   29.2   556   5   US-10-467-903-9        Sequence 9, Appli
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   37   901.5   28.3   559   6   US-11-120-749-24       Sequence 24, Appl
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   39   899.5   28.2   559   5   US-10-287-436A-1245    Sequence 1245, Ap
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   44   892.5   28.0   559   4   US-10-001-851-21       Sequence 21, Appl
   45   892.5   28.0   559   4   US-10-205-219-36       Sequence 36, Appl
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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:59:40 ; Search time 35 Seconds
                                            (without alignments)
                                            1159.690 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLLTVNILVFVG.........VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database :   Published_Applications_AA_New:*
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                 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

          %
Result   Query
No.   Score Match Length DB ID   Description
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    1   3190 100.0   603 7 US-11-312-958-16   Sequence 16, Appl
    2   1077   33.8   297 7 US-11-293-697-2888   Sequence 2888, Ap
    3 895.5   28.1   559 7 US-11-221-332-110   Sequence 110, App
    4   694   21.8   639 6 US-10-196-749-364   Sequence 364, App
    5   471   14.8   372 7 US-11-293-697-2779   Sequence 2779, Ap
    6   154   4.8   28 7 US-11-134-871-1175   Sequence 1175, Ap
    7 115.5   3.6   301 6 US-10-734-719-27   Sequence 27, Appl
    8   113   3.5   303 6 US-10-734-719-29   Sequence 29, Appl
    9 109.5   3.4   646 7 US-11-021-837-58   Sequence 58, Appl
   10   106   3.3   702 7 US-11-178-560-1   Sequence 1, Appli
   11   106   3.3   703 7 US-11-253-453-11   Sequence 11, Appl
   12   106   3.3   972 7 US-11-253-453-1   Sequence 1, Appli
   13   106   3.3   972 7 US-11-233-089-52   Sequence 52, Appl
   14   101   3.2   297 6 US-10-734-719-31   Sequence 31, Appl
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   31   90   2.8   668 7 US-11-056-355B-45266   Sequence 45266, A
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   33   90   2.8 1057 6 US-10-539-228-799   Sequence 799, App
   34   89.5   2.8   270 6 US-10-734-719-39   Sequence 39, Appl
   35   89.5   2.8   415 7 US-11-056-355B-38748   Sequence 38748, A
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   37   89.5   2.8   415 7 US-11-056-355B-78318   Sequence 78318, A
   38   89.5   2.8   415 7 US-11-056-355B-98701   Sequence 98701, A
   39   89.5   2.8   415 7 US-11-056-355B-109940   Sequence 109940,
   40   89.5   2.8   416 7 US-11-056-355B-38747   Sequence 38747, A
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   43   89.5   2.8   416 7 US-11-056-355B-98700   Sequence 98700, A
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45   89.5   2.8   450 7 US-11-056-355B-38746   Sequence 38746, A

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OM protein - protein search, using sw model

Run on: August 16, 2006, 00:41:10 ; Search time 43 Seconds
                                            (without alignments)
                                            1349.272 Million cell updates/sec

Title: US-10-713-345-2
Perfect score: 3190
Sequence: 1 MAVARKIRTLLTVNILVFVG..........VQRCSGQKWMIRNWIKHARH 603

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   906.5 28.4   559   2 A45987   polypeptide N-acet
     2   899.5 28.2   559   2 JC4223   polypeptide N-acet
     3   878   27.5   612   2 T42243   probable polypepti
     4   869   27.2   563   2 A88515   polypeptide N-acet
     5   868.5 27.2   624   2 T42247   polypeptide N-acet
     6   866.5 27.2   626   2 T42246   polypeptide N-acet
     7   857   26.9   623   2 T42245   probable polypepti
     8   796   25.0   589   2 T42244   probable polypepti
     9   794.5 24.9   571   2 I37405   polypeptide N-acet
    10   782   24.5   601   2 T42251   polypeptide N-acet
    11   761.5 23.9   618   2 T42248   polypeptide N-acet
    12   761   23.9   617   2 T42249   polypeptide N-acet
    13   745.5 23.4   579   2 T31549   polypeptide N-acet
    14   744   23.3   633   2 JC5247   polypeptide N-acet
    15   738.5 23.2   562   2 T42250   polypeptide N-acet
    16   735   23.0   605   2 T27397   hypothetical prote
    17   735   23.0   684   2 T26930   hypothetical prote
    18   610.5 19.1   421   2 T42252   polypeptide N-acet
    19   362   11.3   133   2 T46260   hypothetical prote
    20   220.5   6.9   276   2 T12552   hypothetical prote
    21   151.5   4.7   470   2 C70641   hypothetical prote
    22   147.5   4.6   324   2 A69290   probable glycosyl
    23   134.5   4.2   525   2 A45053   proteinase RPI - R
    24   126.5   4.0   302   2 A84263   hypothetical prote
    25   119.5   3.7   697   2 JN0602   rfb protein - Esch
    26   118   3.7   1405   1 S13421   polymeric globin a
    27   117   3.7   726   2 A47275   transferrin - cock
    28   117   3.7   1275   2 T18556   O-antigen biosynth
    29   113.5   3.6   1044   2 H97186   glycosyltransferas
    30   113   3.5   303   2 F81318   probable galactosy
    31   112   3.5   324   2 AB2190   hypothetical prote
    32   107.5   3.4   439   2 AF2602   nicotinate phospho
    33   107.5   3.4   439   2 F97384   nicotinate phospho
    34   107   3.4   313   2 AI2202   hypothetical prote
    35   107   3.4   377   2 JC7535   chitinase (EC 3.2.
    36   106   3.3   972   2 T09595   glucuronosyltransf
    37   105   3.3   328   2 B84263   succinoglycan bios
    38   104   3.3   348   2 T13320   hypothetical prote
    39   104   3.3   503   2 B84007   cardiolipin synthe
    40   103.5   3.2   362   2 G75191   dolichol-phosphate
    41   103   3.2   348   2 T13625   hypothetical prote
    42   103   3.2   685   2 AH3414   soluble lytic mure
    43   101   3.2   293   2 AB3124   glycosyltransferas
    44   101   3.2   293   2 G98163   dtdP-rha, A-D-glcn
    45   101   3.2   787   2 H98163   hypothetical prote

43	931.5	29.2	556	9	ADX58181	Adx58181 Human pol
44	931.5	29.2	556	10	AEF65468	Aef65468 Human GAL
45	931.5	29.2	557	7	ADB76895	Adb76895 Human N-a

```
GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          August 16, 2006, 00:37:44 ; Search time 303 Seconds
                                            (without alignments)
                                            1840.873 Million cell updates/sec

Title:           US-10-713-345-2
Perfect score:   3190
Sequence:        1 MAVARKIRTLLTVNILVFVG..........VQRCSGQKWMIRNWIKHARH 603

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_7.2:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                %
Result        Query
  No.   Score Match Length DB  ID                  Description
------------------------------------------------------------------------
     1   3179  99.7    603  1  GALT9_HUMAN         Q9hcq5 h polypepti
     2 2876.5  90.2    606  1  GALT9_MACFA         Q9gm01 m polypepti
     3 2052.5  64.3    598  1  GLTL3_HUMAN         Q6is24 h putative
     4 2052.5  64.3    598  2  Q2L4S5_HUMAN        Q2l4s5 homo sapien
     5 2051.5  64.3    598  1  GLTL3_MOUSE         Q7ttl5 m putative
     6 2051.5  64.3    598  2  Q59J92_MOUSE        Q59j92 mus musculu
     7 2047.5  64.2    598  2  Q58A53_HUMAN        Q58a53 homo sapien
     8 2047.5  64.2    598  2  Q5CD99_RAT          Q5cd99 rattus norv
     9   1929  60.5    611  2  Q4RFU6_TETNG        Q4rfu6 tetraodon n
    10 1757.5  55.1    554  2  Q4RPK0_TETNG        Q4rpk0 tetraodon n
    11   1586  49.7    607  2  Q58A54_HUMAN        Q58a54 homo sapien
    12   1584  49.7    607  2  Q59J91_MOUSE        Q59j91 mus musculu
    13   1581  49.6    607  1  GLTL4_HUMAN         Q6p9a2 h putative
    14 1566.5  49.1    622  1  GLTL4_MOUSE         Q8k1b9 m putative
    15 1390.5  43.6    534  2  Q4SVX6_TETNG        Q4svx6 tetraodon n
    16   1328  41.6    266  2  Q52LR8_HUMAN        Q521r8 homo sapien
    17   1319  41.3    637  1  GALT8_HUMAN         Q9ny28 h probable
    18   1243  39.0    237  2  Q3TB05_MOUSE        Q3tb05 mus musculu
    19 1230.5  38.6    462  2  Q5RI00_BRARE        Q5ri00 brachydanio
    20   1166  36.6    423  2  Q5RHZ9_BRARE        Q5rhz9 brachydanio
    21 1085.5  34.0    530  2  Q4SKF7_TETNG        Q4skf7 tetraodon n
    22    949  29.7    177  2  Q68VJ2_HUMAN        Q68vj2 homo sapien
    23  932.5  29.2    556  1  GLT13_MOUSE         Q8cf93 m polypepti
    24  932.5  29.2    556  1  GLT13_RAT           Q6ue39 r polypepti
    25  931.5  29.2    556  1  GLT13_HUMAN         Q8iuc8 h polypepti
    26  931.5  29.2    556  2  Q68VI8_HUMAN        Q68vi8 homo sapien
    27  931.5  29.2    556  2  Q6GM51_XENLA        Q6gm51 xenopus lae
    28  910.5  28.5    559  2  Q5ZJL1_CHICK        Q5zjl1 gallus gall
    29  906.5  28.4    559  1  GALT1_BOVIN         Q07537 b polypepti
    30  901.5  28.3    559  1  GALT1_MOUSE         O08912 m polypepti
    31  901.5  28.3    559  1  GALT1_PIG           Q29121 s polypepti
    32  901.5  28.3    559  2  Q5BKS3_MOUSE        Q5bks3 mus musculu
    33  899.5  28.2    559  1  GALT1_HUMAN         Q10472 h polypepti
    34  893.5  28.0    559  2  Q6PA81_XENLA        Q6pa81 xenopus lae
    35  892.5  28.0    559  1  GALT1_RAT           Q10473 r polypepti
    36    878  27.5    612  1  GALT3_CAEEL         P34678 caenorhabdi
    37  875.5  27.4    611  2  Q61DZ1_CAEBR        Q61dz1 caenorhabdi
    38    871  27.3    630  1  GALT5_DROME         Q6wvl7 drosophila
    39  862.5  27.0    626  1  GALT5_CAEEL         Q95zj1 caenorhabdi
    40    862  27.0    404  2  Q4SIA0_TETNG        Q4sia0 tetraodon n
    41    862  27.0    632  2  Q4RQL8_TETNG        Q4rql8 tetraodon n
    42    861  27.0    603  2  Q68F39_XENLA        Q68f39 xenopus lae
    43    858  26.9    563  2  Q6DJR8_XENTR        Q6djr8 xenopus tro
    44    853  26.7    578  1  GALT4_HUMAN         Q8n4a0 h polypepti
    45    853  26.7    608  1  GLT11_MOUSE         Q92118 m polypepti
```

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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 00:45:58 ; Search time 14669.9 Seconds
                                          (without alignments)
                                          11211.577 Million cell updates/sec

Title:         US-10-713-345-1
Perfect score: 2572
Sequence:      1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:     12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     GenEmbl:*
               1: gb_env:*
               2: gb_pat:*
               3: gb_ph:*
               4: gb_pl:*
               5: gb_pr:*
               6: gb_ro:*
               7: gb_sts:*
               8: gb_sy:*
               9: gb_un:*
               10:  gb_vi:*
               11:  gb_ov:*
               12:  gb_htg:*
               13:  gb_in:*
               14:  gb_om:*
               15:  gb_ba:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result          Query
  No.   Score  Match Length DB  ID                 Description
-------------------------------------------------------------------------
     1    2572 100.0   2572  2  AR483255           AR483255 Sequence
     2  2006.2  78.0   2183  5  AK055773           AK055773 Homo sapi
     3    1980  77.0   2535  5  AB050509           AB050509 Macaca fa
     4    1812  70.5   1812  2  AR483256           AR483256 Sequence
     5  1805.6  70.2   1812  5  AB040672           AB040672 Homo sapi
     6  1171.4  45.5   1727  2  AX713432           AX713432 Sequence
     7  1171.4  45.5   1727  5  AK054820           AK054820 Homo sapi
     8    1171  45.5   1742  5  AF458594           AF458594 Homo sapi
     9   786.6  30.6   3439  2  AX574388           AX574388 Sequence
    10   784.8  30.5   3333  2  AX544488           AX544488 Sequence
    11   783.4  30.5   1797  2  AX544489           AX544489 Sequence
    12   783.4  30.5   1797  5  AJ626726           AJ626726 Homo sapi
    13   783.4  30.5   1945  5  BC069624           BC069624 Homo sapi
    14   783.4  30.5   1945  5  BC069628           BC069628 Homo sapi
    15   783.4  30.5   1945  5  BC069636           BC069636 Homo sapi
    16   783.4  30.5   3298  5  AF410457           AF410457 Homo sapi
    17   781.8  30.4   1945  5  BC069645           BC069645 Homo sapi
    18   781.8  30.4   1994  5  BC067524           BC067524 Homo sapi
    19   781.8  30.4   1994  5  BC067525           BC067525 Homo sapi
    20   781.8  30.4   1994  5  BC069997           BC069997 Homo sapi
    21   778.6  30.3   1797  5  AB078148           AB078148 Homo sapi
    22   771.4  30.0   1797  6  AB040671           AB040671 Rattus no
    23    769   29.9    836  5  BC093817           BC093817 Homo sapi
    24    769   29.9    836  5  BC093819           BC093819 Homo sapi
    25   756.8  29.4   3580  6  BC052469           BC052469 Mus muscu
    26   756.8  29.4   4132  6  BC069177           BC069177 Mus muscu
    27   755.4  29.4   1797  6  AB175684           AB175684 Mus muscu
    28   748.4  29.1   3653  2  CQ843080           CQ843080 Sequence
    29   748.4  29.1   3653  5  AK126044           AK126044 Homo sapi
    30   744.2  28.9   3183  2  CS167200           CS167200 Sequence
    31   744.2  28.9   3183  2  AX833321           AX833321 Sequence
    32   744.2  28.9   3183  5  AK094958           AK094958 Homo sapi
    33    738   28.7   2278  6  AF467979           AF467979 Mus muscu
    34    658   25.6    658  2  CQ724811           CQ724811 Sequence
 c  35   589.2  22.9    664  5  HSA339305          AJ339305 Homo sapi
 c  36   589.2  22.9 129492  5  AC138466           AC138466 Homo sapi
    37    588   22.9   2496  2  AX713553           AX713553 Sequence
```

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38     588   22.9   2496  5  AK055111              AK055111 Homo sapi
39     588   22.9   2519  5  BC060864              BC060864 Homo sapi
40     588   22.9   2520  5  BC037341              BC037341 Homo sapi
41     588   22.9   2534  2  AX451430              AX451430 Sequence
42   587.2   22.8   1824  6  AB175685              AB175685 Mus muscu
43   586.6   22.8   1824  5  AB078147              AB078147 Homo sapi
44   586.6   22.8   1824  5  AJ626724              AJ626724 Homo sapi
45   579.2   22.5   1981  5  AB050513              AB050513 Macaca fa
```

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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 00:44:33 ; Search time 1619.23 Seconds
                                          (without alignments)
                                          11074.760 Million cell updates/sec

Title:         US-10-713-345-1
Perfect score: 2572
Sequence:      1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_8:*
               1:  geneseqn1980s:*
               2:  geneseqn1990s:*
               3:  geneseqn2000s:*
               4:  geneseqn2001as:*
               5:  geneseqn2001bs:*
               6:  geneseqn2002as:*
               7:  geneseqn2002bs:*
               8:  geneseqn2003as:*
               9:  geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*
               15: geneseqn2006s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                            SUMMARIES
                  %
Result          Query
  No.    Score   Match  Length  DB   ID              Description
----------------------------------------------------------------------------
    1     2572   100.0    2572   8   ABX14500        Abx14500 cDNA enco
    2     2572   100.0    2572  10   ADC77652        Adc77652 Human 471
    3     2572   100.0    2572  12   ADM46165        Adm46165 cDNA enco
    4   2241.6    87.2    2410  12   ADQ24697        Adq24697 Human sof
    5     1812    70.5    1812  12   ADM46167        Adm46167 ORF of cD
    6   1386.4    53.9    1525   4   AAI59554        Aai59554 Human pol
    7   1171.4    45.5    1727  10   ADA52548        Ada52548 Human cod
    8   1131.6    44.0    1322   5   ABA11363        Aba11363 Human ner
    9    952.8    37.0     956   4   AAI61340        Aai61340 Human pol
   10    797.4    31.0     799   3   AAC75948        Aac75948 Human ORF
   11    786.6    30.6    3439   6   ABK91321        Abk91321 cDNA enco
   12    784.8    30.5    3333   6   ABV85011        Abv85011 Human pp-
   13    783.4    30.5    1797   6   ABV85012        Abv85012 Human pp-
   14    778.6    30.3    1797  10   ADC35397        Adc35397 Human N-a
   15    778.4    30.3    2557  13   ADS10210        Ads10210 Human the
   16    773.8    30.1    1915   4   AAI60831        Aai60831 Human pol
   17    748.4    29.1    3653  12   ADQ64566        Adq64566 Novel hum
   18    744.2    28.9    3183  11   ADM01760        Adm01760 Human cDN
   19    744.2    28.9    3183  14   AEC84690        Aec84690 Human cDN
   20    689.4    26.8    3109  10   ADE47679        Ade47679 Human NOV
   21    689.4    26.8    3109  12   ADJ78949        Adj78949 Human NOV
   22    689.4    26.8    3109  12   ADJ71668        Adj71668 Human NOV
   23    689.4    26.8    3109  12   ADJ71660        Adj71660 Human NOV
   24    689.4    26.8    3109  12   ADJ71666        Adj71666 Human NOV
   25    687.8    26.7    3109  12   ADJ71664        Adj71664 Human NOV
   26    639.8    24.9    1306  12   ADJ71662        Adj71662 Human NOV
   27    634.4    24.7     982   5   ABA11032        Aba11032 Human ner
   28     588     22.9    2496  10   ADA52669        Ada52669 Human cod
   29     588     22.9    2519   9   ACH04034        Ach04034 Human cDN
   30     588     22.9    2534   6   AAD35232        Aad35232 Human TRN
   31    586.6    22.8    1824  10   ADC35396        Adc35396 Human N-a
   32    584.8    22.7    2422  10   ADE47689        Ade47689 Human NOV
   33    584.8    22.7    2422  10   ADE47687        Ade47687 Human NOV
   34    584.8    22.7    2422  10   ADE47685        Ade47685 Human NOV
   35    584.8    22.7    2422  12   ADJ78957        Adj78957 Human NOV
   36    584.8    22.7    2422  12   ADJ78955        Adj78955 Human NOV
   37    584.8    22.7    2422  12   ADJ78959        Adj78959 Human NOV
```

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     38   532.4   20.7    534  10  ADE25971          Ade25971 N-acetylg
     39   532.4   20.7    534  14  ADX58234          Adx58234 Human pol
 c   40    505    19.6    505  12  ADQ20725          Adq20725 Human sof
     41   476.2   18.5   2465  10  ADB62317          Adb62317 Human cDN
     42   424.4   16.5   2388   4  AAI60021         Aai60021 Human pol
     43   424.4   16.5   2388  13  ADS11539          Ads11539 Human the
     44   422.8   16.4   2416   4  AAI58235         Aai58235 Human pol
     45   422.8   16.4   2416   5  ADQ98442          Adq98442 DNA encod
```

```
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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 01:13:47 ; Search time 480.49 Seconds
                                              (without alignments)
                                         10015.801 Million cell updates/sec

Title:           US-10-713-345-1
Perfect score:   2572
Sequence:        1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:       2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result          Query
   No.   Score   Match Length DB  ID                    Description
-------------------------------------------------------------------------------
       1    2572  100.0   2572  3  US-09-973-457-1       Sequence 1, Appli
       2    1812   70.5   1812  3  US-09-973-457-3       Sequence 3, Appli
       3  1171.4   45.5   1727  4  US-10-094-749-116     Sequence 116, App
       4     588   22.9   2496  4  US-10-094-749-237     Sequence 237, App
       5   476.2   18.5   2465  3  US-10-104-047-471     Sequence 471, App
       6   422.8   16.4   2416  3  US-09-620-312D-112    Sequence 112, App
       7     368   14.3    903  3  US-09-620-312D-938    Sequence 938, App
       8   222.4    8.6   2199  3  US-09-799-451-328     Sequence 328, App
       9   208.4    8.1   1540  3  US-09-270-767-11959   Sequence 11959, A
      10   204.2    7.9   1920  3  US-09-376-856-1       Sequence 1, Appli
      11   204.2    7.9   2575  3  US-10-012-231A-346    Sequence 346, App
      12   204.2    7.9   2575  3  US-10-015-389A-346    Sequence 346, App
      13   204.2    7.9   2575  3  US-10-006-768A-346    Sequence 346, App
      14   204.2    7.9   2575  3  US-10-015-671A-346    Sequence 346, App
      15   204.2    7.9   2575  3  US-10-015-393A-346    Sequence 346, App
      16   204.2    7.9   2575  3  US-10-011-833A-346    Sequence 346, App
      17   204.2    7.9   2575  3  US-10-006-041A-346    Sequence 346, App
      18   204.2    7.9   2575  3  US-10-012-064A-346    Sequence 346, App
      19   204.2    7.9   2575  4  US-10-015-392A-346    Sequence 346, App
      20   204.2    7.9   2575  5  US-10-011-795B-346    Sequence 346, App
      21   204.2    7.9   2575  5  US-10-015-386A-346    Sequence 346, App
      22   204.2    7.9   2575  5  US-10-012-121A-346    Sequence 346, App
      23   204.2    7.9   2575  5  US-10-006-485A-346    Sequence 346, App
      24   204.2    7.9   2575  5  US-10-006-746A-346    Sequence 346, App
      25   204.2    7.9   2575  5  US-10-012-752A-346    Sequence 346, App
      26   204.2    7.9   2575  5  US-10-017-253A-346    Sequence 346, App
      27   204.2    7.9   2575  5  US-10-015-519A-346    Sequence 346, App
      28   204.2    7.9   2575  5  US-10-015-715A-346    Sequence 346, App
      29   204.2    7.9   2575  5  US-10-007-236A-346    Sequence 346, App
      30   203.2    7.9   2095  3  US-10-104-047-435     Sequence 435, App
      31   202.6    7.9   3332  3  US-09-347-488-1       Sequence 1, Appli
      32     190    7.4    740  3  US-09-270-767-27636   Sequence 27636, A
      33   186.4    7.2   1521  3  US-09-795-926-30      Sequence 30, Appl
      34   186.4    7.2   1521  3  US-10-364-774-30      Sequence 30, Appl
      35   186.4    7.2   1812  3  US-09-795-926-42      Sequence 42, Appl
      36   186.4    7.2   1812  3  US-10-364-774-42      Sequence 42, Appl
      37   186.4    7.2   3896  3  US-09-795-926-44      Sequence 44, Appl
      38   186.4    7.2   3896  3  US-10-364-774-44      Sequence 44, Appl
      39   171.6    6.7   1746  3  US-10-074-527-3       Sequence 3, Appli
      40   171.6    6.7   2850  3  US-10-074-527-1       Sequence 1, Appli
  c   41   154.6    6.0    910  3  US-09-270-767-2104    Sequence 2104, Ap
  c   42   154.6    6.0    910  3  US-09-270-767-17386   Sequence 17386, A
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c  43   144.4   5.6    868   3  US-09-270-767-13764      Sequence 13764, A
   44   137.4   5.3   1771   3  US-09-976-594-28         Sequence 28, Appl
   45   133.2   5.2    810   3  US-09-795-926-26         Sequence 26, Appl
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:        August 17, 2006, 01:42:59 ; Search time 4212.94 Seconds
                                          (without alignments)
                                          7501.600 Million cell updates/sec

Title:         US-10-713-345-1
Perfect score: 2572
Sequence:      1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                      %
Result             Query
   No.    Score  Match Length DB  ID                        Description
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     2    2572   100.0   2572  7   US-10-369-022-15         Sequence 15, Appl
     3    2572   100.0   2572  7   US-10-184-648-42         Sequence 42, Appl
     4    2572   100.0   2572  8   US-10-713-345-1          Sequence 1, Appli
     5  2241.6    87.2   2410  9   US-10-723-860-7517       Sequence 7517, Ap
     6    1812    70.5   1812  3   US-09-973-457-3          Sequence 3, Appli
     7    1812    70.5   1812  7   US-10-184-648-44         Sequence 44, Appl
     8    1812    70.5   1812  8   US-10-713-345-3          Sequence 3, Appli
     9  1171.4    45.5   1727  7   US-10-094-749-116        Sequence 116, App
    10   786.6    30.6   3439  9   US-10-467-903-21         Sequence 21, Appl
    11   784.8    30.5   3333  6   US-10-060-895A-1         Sequence 1, Appli
    12   783.4    30.5   1797  6   US-10-060-895A-2         Sequence 2, Appli
    13   744.2    28.9   3183  7   US-10-108-260A-445       Sequence 445, App
    14   689.4    26.8   3109  8   US-10-210-130-41         Sequence 41, Appl
    15   689.4    26.8   3109  9   US-10-635-398-61         Sequence 61, Appl
    16   689.4    26.8   3109  9   US-10-635-398-67         Sequence 67, Appl
    17   689.4    26.8   3109  9   US-10-635-398-69         Sequence 69, Appl
    18   687.8    26.7   3109  9   US-10-635-398-65         Sequence 65, Appl
    19   639.8    24.9   1306  9   US-10-635-398-63         Sequence 63, Appl
    20    588     22.9   2496  7   US-10-094-749-237        Sequence 237, App
    21    588     22.9   2519  6   US-10-116-802-239        Sequence 239, App
    22    588     22.9   2534  7   US-10-288-252-37         Sequence 37, Appl
    23    588     22.9   2534  8   US-10-398-038-37         Sequence 37, Appl
    24    588     22.9   2534  10  US-10-976-440-37         Sequence 37, Appl
    25   584.8    22.7   2422  8   US-10-210-130-47         Sequence 47, Appl
    26   584.8    22.7   2422  8   US-10-210-130-49         Sequence 49, Appl
    27   584.8    22.7   2422  8   US-10-210-130-51         Sequence 51, Appl
    28   532.4    20.7    534  7   US-10-292-896-115        Sequence 115, App
    29   532.4    20.7    534  9   US-10-705-401-112        Sequence 112, App
  c 30    505     19.6    505  9   US-10-723-860-3545       Sequence 3545, Ap
    31   476.2    18.5   2465  7   US-10-104-047-471        Sequence 471, App
    32   476.2    18.5   2465  16  US-11-072-512-471        Sequence 471, App
    33   422.8    16.4   2416  6   US-10-037-270-112        Sequence 112, App
    34   422.8    16.4   2416  7   US-10-117-722-112        Sequence 112, App
    35   422.8    16.4   2416  10  US-10-122-851-112        Sequence 112, App
    36   402.2    15.6    453  3   US-09-918-995-28101      Sequence 28101, A
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37	368	14.3	903	6	US-10-037-270-938	Sequence 938, App
38	368	14.3	903	7	US-10-117-722-938	Sequence 938, App
39	368	14.3	903	10	US-10-122-851-938	Sequence 938, App
40	354.4	13.8	1271	8	US-10-276-723-1	Sequence 1, Appli
41	334.8	13.0	580	8	US-10-210-130-43	Sequence 43, Appl
42	293.4	11.4	793	6	US-10-060-895A-4	Sequence 4, Appli
43	292	11.4	757	6	US-10-060-895A-6	Sequence 6, Appli
44	235.6	9.2	1869	9	US-10-789-241-47	Sequence 47, Appl
45	235.6	9.2	1869	10	US-10-756-149-1870	Sequence 1870, Ap

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OM nucleic - nucleic search, using sw model

Run on:         August 17, 2006, 01:59:47 ; Search time 451.156 Seconds
                                            (without alignments)
                                            9113.283 Million cell updates/sec

Title:          US-10-713-345-1
Perfect score:  2572
Sequence:       1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters:      4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA_New:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                    %
Result          Query
    No.   Score  Match Length DB  ID                    Description
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      3   744.2   28.9   3183  8  US-11-293-697-445      Sequence 445, App
      4    588    22.9   2519  8  US-11-266-748A-31678   Sequence 31678, A
      5    588    22.9   2519  8  US-11-266-748A-56113   Sequence 56113, A
      6    454    17.7    794  8  US-11-266-748A-1713    Sequence 1713, Ap
      7    370    14.4   2135  8  US-11-266-748A-23941   Sequence 23941, A
      8    370    14.4   2135  8  US-11-266-748A-57086   Sequence 57086, A
      9   316.2   12.3    920  8  US-11-266-748A-190028  Sequence 190028,
     10   238.2    9.3   1000  8  US-11-266-748A-406202  Sequence 406202,
c    11   238.2    9.3   1000  8  US-11-266-748A-477248  Sequence 477248,
c    12   235.6    9.2   2332  8  US-11-266-748A-189071  Sequence 189071,
     13   235.6    9.2   2332  8  US-11-266-748A-242737  Sequence 242737,
     14   235.6    9.2   2819  8  US-11-266-748A-27039   Sequence 27039, A
     15   204.2    7.9   2575  6  US-10-196-749-363      Sequence 363, App
     16   204.2    7.9   3580  8  US-11-266-748A-56877   Sequence 56877, A
     17   186.4    7.2   5222  8  US-11-266-748A-31657   Sequence 31657, A
     18   184.4    7.2   3105  8  US-11-293-697-336      Sequence 336, App
     19   173.8    6.8   1163  8  US-11-266-748A-367663  Sequence 367663,
c    20   173.8    6.8   1163  8  US-11-266-748A-451042  Sequence 451042,
     21    170     6.6   1746  8  US-11-266-748A-22604   Sequence 22604, A
     22   165.4    6.4   1542  8  US-11-266-748A-188164  Sequence 188164,
     23   165.4    6.4   4464  8  US-11-266-748A-27336   Sequence 27336, A
     24   164.4    6.4    650  7  US-11-190-172-4285     Sequence 4285, Ap
     25   151.8    5.9   1140  8  US-11-266-748A-96859   Sequence 96859, A
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c    29   128.4    5.0    968  8  US-11-266-748A-370880  Sequence 370880,
     30   128.4    5.0    968  8  US-11-266-748A-454259  Sequence 454259,
     31   119.8    4.7   2185  8  US-11-221-332-109      Sequence 109, App
     32    117     4.5    818  8  US-11-266-748A-356278  Sequence 356278,
     33    117     4.5    818  8  US-11-266-748A-385814  Sequence 385814,
c    34    117     4.5    818  8  US-11-266-748A-439657  Sequence 439657,
c    35    111     4.3    769  8  US-11-266-748A-259798  Sequence 259798,
c    36    111     4.3    769  8  US-11-266-748A-279021  Sequence 279021,
     37    111     4.3    769  8  US-11-266-748A-320315  Sequence 320315,
     38    104     4.0   1000  8  US-11-266-748A-399106  Sequence 399106,
c    39    104     4.0   1000  8  US-11-266-748A-470152  Sequence 470152,
     40   103.8    4.0   1066  8  US-11-266-748A-360857  Sequence 360857,
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   44    96.4   3.7    869  8  US-11-266-748A-98384       Sequence 98384, A
c  45    96.4   3.7    869  8  US-11-266-748A-151195      Sequence 151195,
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OM nucleic - nucleic search, using sw model

Run on:         August 17, 2006, 00:50:04 ; Search time 12286.2 Seconds
                                             (without alignments)
                                             11706.157 Million cell updates/sec

Title:          US-10-713-345-1
Perfect score:  2572
Sequence:       1 gcgccgcccgcccgcgcctt..........cccccagcacttgcggccgc 2572

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:     96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      EST:*
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                10: gb_est9:*
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                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                  %
Result          Query
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    3   838.8   32.6   1056   3  BM925654        BM925654 AGENCOURT
    4   813.2   31.6   1322  14  DQ048171        DQ048171 Pan trogl
    5   783.4   30.5   1797  14  AY407808        AY407808 Homo sapi
    6   755.4   29.4   1797  14  AY407810        AY407810 Mus muscu
    7   732     28.5    879   2  BI756878        BI756878 603029069
    8   720.4   28.0    866  10  DV913368        DV913368 LB02827.C
    9   717.6   27.9   1120   3  BM907000        BM907000 AGENCOURT
   10   702     27.3    761   2  BI822362        BI822362 603037922
   11   678.6   26.4    806   8  CO886915        CO886915 BovGen_15
   12   675.6   26.3    839   5  CJ470325        CJ470325 CJ470325
   13   655     25.5    655   4  BX099049        BX099049 BX099049
   14   645     25.1   1016  10  DV011836        DV011836 CNB271-C0
   15   620.8   24.1    624   4  CB152086        CB152086 K-EST0209
   16   616.8   24.0    782   8  CN823582        CN823582 Oa_splbn_
   17   611.8   23.8   2031   6  AK048758        AK048758 Mus muscu
   18   604.8   23.5    652   5  CD630910        CD630910 56006229J
   19   602.4   23.4   1797  14  AY407809        AY407809 Pan trogl
   20   598.2   23.3    793   2  BI552481        BI552481 603196186
   21   595.2   23.1   1990   6  AK035817        AK035817 Mus muscu
   22   592.4   23.0   2617   6  AK051281        AK051281 Mus muscu
   23   591.8   23.0   1541   6  AK171529        AK171529 Mus muscu
   24   588.4   22.9    596   9  DR001000        DR001000 TC112896
   25   588     22.9    588   9  DA406079        DA406079 DA406079
   26   582.4   22.6    596   9  DA586340        DA586340 DA586340
   27   580     22.6    580   9  DA064328        DA064328 DA064328
   28   574.4   22.3    576   9  DA079387        DA079387 DA079387
   29   574     22.3    574   9  DA086071        DA086071 DA086071
   30   568.4   22.1    575   9  DA206384        DA206384 DA206384
   31   564     21.9    564   9  DA077079        DA077079 DA077079
   32   561     21.8    561   9  DA201413        DA201413 DA201413
   33   560.4   21.8    562   9  DA355587        DA355587 DA355587
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	39	519	20.2	555	9	DA074160	DA074160	DA074160
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	41	516.6	20.1	1046	10	DW666789	DW666789	CNB338-H1
	42	513.4	20.0	525	9	DA624069	DA624069	DA624069
	43	512.8	19.9	517	4	CB153078	CB153078	K-EST0210
	44	506.4	19.7	780	3	BU385765	BU385765	603861678
c	45	505	19.6	505	7	AW294162	AW294162	UI-H-BI2-

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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 00:45:58 ; Search time 10335.1 Seconds
                                             (without alignments)
                                             11211.577 Million cell updates/sec

Title:           US-10-713-345-3
Perfect score:   1812
Sequence:        1 atggcggtggccaggaagat..........tcaaacacgcacggcactga 1812

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                   %
Result           Query
 No.    Score  Match Length DB   ID                 Description
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    3  1805.6   99.6   1812   5   AB040672           AB040672 Homo sapi
    4  1570.2   86.7   2183   5   AK055773           AK055773 Homo sapi
    5  1549.4   85.5   2535   5   AB050509           AB050509 Macaca fa
    6   783.4   43.2   1797   2   AX544489           AX544489 Sequence
    7   783.4   43.2   1797   5   AJ626726           AJ626726 Homo sapi
    8   783.4   43.2   1945   5   BC069624           BC069624 Homo sapi
    9   783.4   43.2   1945   5   BC069628           BC069628 Homo sapi
   10   783.4   43.2   1945   5   BC069636           BC069636 Homo sapi
   11   783.4   43.2   3298   5   AF410457           AF410457 Homo sapi
   12   783.4   43.2   3333   2   AX544488           AX544488 Sequence
   13   783.4   43.2   3439   2   AX574388           AX574388 Sequence
   14   781.8   43.1   1945   5   BC069645           BC069645 Homo sapi
   15   781.8   43.1   1994   5   BC067524           BC067524 Homo sapi
   16   781.8   43.1   1994   5   BC067525           BC067525 Homo sapi
   17   781.8   43.1   1994   5   BC069997           BC069997 Homo sapi
   18   778.6   43.0   1797   5   AB078148           AB078148 Homo sapi
   19   771.4   42.6   1797   6   AB040671           AB040671 Rattus no
   20   755.4   41.7   1797   6   AB175684           AB175684 Mus muscu
   21   755.4   41.7   3580   6   BC052469           BC052469 Mus muscu
   22   755.4   41.7   4132   6   BC069177           BC069177 Mus muscu
   23   748.4   41.3   3653   2   CQ843080           CQ843080 Sequence
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   25   744.2   41.1   3183   2   CS167200           CS167200 Sequence
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   27   744.2   41.1   3183   5   AK094958           AK094958 Homo sapi
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   29   735.4   40.6   1727   2   AX713432           AX713432 Sequence
   30   735.4   40.6   1727   5   AK054820           AK054820 Homo sapi
   31    735    40.6    836   5   BC093817           BC093817 Homo sapi
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   33    735    40.6   1742   5   AF458594           AF458594 Homo sapi
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   35   587.2   32.4   1824   6   AB175685           AB175685 Mus muscu
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38	586.6	32.4	2496	2	AX713553	AX713553 Sequence
39	586.6	32.4	2496	5	AK055111	AK055111 Homo sapi
40	586.6	32.4	2519	5	BC060864	BC060864 Homo sapi
41	586.6	32.4	2520	5	BC037341	BC037341 Homo sapi
42	586.6	32.4	2534	2	AX451430	AX451430 Sequence
43	579.2	32.0	1981	5	AB050513	AB050513 Macaca fa
44	533.8	29.5	2595	6	BC024988	BC024988 Mus muscu
45	532.4	29.4	534	2	CQ816194	CQ816194 Sequence

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 00:44:33 ; Search time 1140.77 Seconds
                                          (without alignments)
                                          11074.760 Million cell updates/sec

Title:           US-10-713-345-3
Perfect score:   1812
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:     10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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       Pred. No. is the number of results predicted by chance to have a
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       and is derived by analysis of the total score distribution.

                             SUMMARIES
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     4    1812   100.0   2572  12  ADM46165         Adm46165 cDNA enco
     5  1805.6    99.6   2410  12  ADQ24697         Adq24697 Human sof
     6  1155.8    63.8   1525   4  AAI59554         Aai59554 Human pol
     7  1051.4    58.0   1322   5  ABA11363         Aba11363 Human ner
     8   944.8    52.1    956   4  AAI61340         Aai61340 Human pol
     9   797.4    44.0    799   3  AAC75948         Aac75948 Human ORF
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    12   783.4    43.2   3439   6  ABK91321         Abk91321 cDNA enco
    13   778.6    43.0   1797  10  ADC35397         Adc35397 Human N-a
    14   777.8    42.9   2557  13  ADS10210         Ads10210 Human the
    15   773.8    42.7   1915   4  AAI60831         Aai60831 Human pol
    16   748.4    41.3   3653  12  ADQ64566         Adq64566 Novel hum
    17   744.2    41.1   3183  11  ADM01760         Adm01760 Human cDN
    18   744.2    41.1   3183  14  AEC84690         Aec84690 Human cDN
    19   735.4    40.6   1727  10  ADA52548         Ada52548 Human cod
    20   689.4    38.0   3109  10  ADE47679         Ade47679 Human NOV
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    28   586.6    32.4   2496  10  ADA52669         Ada52669 Human cod
    29   586.6    32.4   2519   9  ACH04034         Ach04034 Human cDN
    30   586.6    32.4   2534   6  AAD35232         Aad35232 Human TRN
    31   583.4    32.2   2422  10  ADE47689         Ade47689 Human NOV
    32   583.4    32.2   2422  10  ADE47687         Ade47687 Human NOV
    33   583.4    32.2   2422  10  ADE47685         Ade47685 Human NOV
    34   583.4    32.2   2422  12  ADJ78957         Adj78957 Human NOV
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38   532.4   29.4    534  14  ADX58234           Adx58234 Human pol
39   476.2   26.3   2465  10  ADB62317           Adb62317 Human cDN
40   424.4   23.4   2388   4  AAI60021           Aai60021 Human pol
41   424.4   23.4   2388  13  ADS11539           Ads11539 Human the
42   422.8   23.3   2416   4  AAI58235           Aai58235 Human pol
43   422.8   23.3   2416   5  ADQ98442           Adq98442 DNA encod
44   422.8   23.3   2416   9  ADB48202           Adb48202 Novel hum
45   402.2   22.2    453   9  ACH40889           Ach40889 Human foe
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 01:13:47 ; Search time 338.51 Seconds
                                             (without alignments)
                                             10015.801 Million cell updates/sec

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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result           Query
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       3  735.4   40.6   1727   4  US-10-094-749-116     Sequence 116, App
       4  586.6   32.4   2496   4  US-10-094-749-237     Sequence 237, App
       5  476.2   26.3   2465   3  US-10-104-047-471     Sequence 471, App
       6  422.8   23.3   2416   3  US-09-620-312D-112    Sequence 112, App
       7    368   20.3    903   3  US-09-620-312D-938    Sequence 938, App
       8  222.4   12.3   2199   3  US-09-799-451-328     Sequence 328, App
       9  208.4   11.5   1540   3  US-09-270-767-11959   Sequence 11959, A
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      34  186.4   10.3   1521   3  US-10-364-774-30      Sequence 30, Appl
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 c    41  154.6    8.5    910   3  US-09-270-767-2104    Sequence 2104, Ap
 c    42  154.6    8.5    910   3  US-09-270-767-17386   Sequence 17386, A
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c  43   144.4   8.0    868  3  US-09-270-767-13764      Sequence 13764, A
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                         GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 01:42:59 ; Search time 2968.06 Seconds
                                            (without alignments)
                                            7501.600 Million cell updates/sec

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Perfect score:   1812
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Scoring table:   IDENTITY_NUC
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Searched:        18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:     37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
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                                  SUMMARIES
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            5   1812   100.0   2572   7   US-10-369-022-15      Sequence 15, Appl
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            7   1812   100.0   2572   8   US-10-713-345-1       Sequence 1, Appli
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            9   783.4   43.2   1797   6   US-10-060-895A-2      Sequence 2, Appli
           10   783.4   43.2   3333   6   US-10-060-895A-1      Sequence 1, Appli
           11   783.4   43.2   3439   9   US-10-467-903-21      Sequence 21, Appl
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           13   735.4   40.6   1727   7   US-10-094-749-116     Sequence 116, App
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           15   689.4   38.0   3109   9   US-10-635-398-61      Sequence 61, Appl
           16   689.4   38.0   3109   9   US-10-635-398-67      Sequence 67, Appl
           17   689.4   38.0   3109   9   US-10-635-398-69      Sequence 69, Appl
           18   687.8   38.0   3109   9   US-10-635-398-65      Sequence 65, Appl
           19   639.8   35.3   1306   9   US-10-635-398-63      Sequence 63, Appl
           20   586.6   32.4   2496   7   US-10-094-749-237     Sequence 237, App
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           29   532.4   29.4    534   9   US-10-705-401-112     Sequence 112, App
           30   476.2   26.3   2465   7   US-10-104-047-471     Sequence 471, App
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41    292    16.1    757   6   US-10-060-895A-6         Sequence 6, Appli
42    292    16.1    793   6   US-10-060-895A-4         Sequence 4, Appli
43   235.6   13.0   1869   9   US-10-789-241-47         Sequence 47, Appl
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45   235.6   13.0   2844   6   US-10-098-841-221        Sequence 221, App
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:          August 17, 2006, 01:59:47 ; Search time 317.844 Seconds
                                          (without alignments)
                                          9113.283 Million cell updates/sec

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Scoring table:   IDENTITY_NUC
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Searched:        2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters:     4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
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	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1812	100.0	2572	8	US-11-312-958-15	Sequence 15, Appl
	2	783.4	43.2	3298	8	US-11-266-748A-56451	Sequence 56451, A
	3	744.2	41.1	3183	8	US-11-293-697-445	Sequence 445, App
	4	586.6	32.4	2519	8	US-11-266-748A-31678	Sequence 31678, A
	5	586.6	32.4	2519	8	US-11-266-748A-56113	Sequence 56113, A
	6	454	25.1	794	8	US-11-266-748A-1713	Sequence 1713, Ap
	7	370	20.4	2135	8	US-11-266-748A-23941	Sequence 23941, A
	8	370	20.4	2135	8	US-11-266-748A-57086	Sequence 57086, A
	9	316.2	17.5	920	8	US-11-266-748A-190028	Sequence 190028,
	10	236.8	13.1	1000	8	US-11-266-748A-406202	Sequence 406202,
c	11	236.8	13.1	1000	8	US-11-266-748A-477248	Sequence 477248,
c	12	235.6	13.0	2332	8	US-11-266-748A-189071	Sequence 189071,
	13	235.6	13.0	2332	8	US-11-266-748A-242737	Sequence 242737,
	14	235.6	13.0	2819	8	US-11-266-748A-27039	Sequence 27039, A
	15	204.2	11.3	2575	6	US-10-196-749-363	Sequence 363, App
	16	204.2	11.3	3580	8	US-11-266-748A-56877	Sequence 56877, A
	17	186.4	10.3	5222	8	US-11-266-748A-31657	Sequence 31657, A
	18	184.4	10.2	3105	8	US-11-293-697-336	Sequence 336, App
	19	173.8	9.6	1163	8	US-11-266-748A-367663	Sequence 367663,
c	20	173.8	9.6	1163	8	US-11-266-748A-451042	Sequence 451042,
	21	170	9.4	1746	8	US-11-266-748A-22604	Sequence 22604, A
	22	165.4	9.1	1542	8	US-11-266-748A-188164	Sequence 188164,
	23	165.4	9.1	4464	8	US-11-266-748A-27336	Sequence 27336, A
	24	164.4	9.1	650	7	US-11-190-172-4285	Sequence 4285, Ap
	25	151.8	8.4	1140	8	US-11-266-748A-96859	Sequence 96859, A
c	26	151.8	8.4	1140	8	US-11-266-748A-149670	Sequence 149670,
	27	135.4	7.5	5360	8	US-11-266-748A-57295	Sequence 57295, A
	28	131.4	7.3	1635	8	US-11-266-748A-183850	Sequence 183850,
c	29	128.4	7.1	968	8	US-11-266-748A-370880	Sequence 370880,
	30	128.4	7.1	968	8	US-11-266-748A-454259	Sequence 454259,
	31	119.8	6.6	2185	8	US-11-221-332-109	Sequence 109, App
	32	117	6.5	818	8	US-11-266-748A-356278	Sequence 356278,
	33	117	6.5	818	8	US-11-266-748A-385814	Sequence 385814,
c	34	117	6.5	818	8	US-11-266-748A-439657	Sequence 439657,
c	35	111	6.1	769	8	US-11-266-748A-259798	Sequence 259798,
c	36	111	6.1	769	8	US-11-266-748A-279021	Sequence 279021,
	37	111	6.1	769	8	US-11-266-748A-320315	Sequence 320315,
	38	104	5.7	1000	8	US-11-266-748A-399106	Sequence 399106,
c	39	104	5.7	1000	8	US-11-266-748A-470152	Sequence 470152,
	40	103.8	5.7	1066	8	US-11-266-748A-360857	Sequence 360857,
c	41	103.8	5.7	1066	8	US-11-266-748A-444236	Sequence 444236,
	42	103	5.7	862	8	US-11-266-748A-98276	Sequence 98276, A

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c  43      103    5.7    862  8  US-11-266-748A-151087      Sequence 151087,
   44     96.4    5.3    869  8  US-11-266-748A-98384       Sequence 98384, A
c  45     96.4    5.3    869  8  US-11-266-748A-151195      Sequence 151195,
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 00:50:04 ; Search time 8655.77 Seconds
                                            (without alignments)
                                            11706.157 Million cell updates/sec

Title: US-10-713-345-3
Perfect score: 1812
Sequence: 1 atggcggtggccaggaagat..........tcaaacacgcacggcactga 1812

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                10: gb_est9:*
                11: gb_gss1:*
                12: gb_gss2:*
                13: gb_gss3:*
                14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB   ID   Description
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     1 1373.8   75.8   2886   6   AK032568   AK032568 Mus muscu
     2 1180.8   65.2   1368 14   DQ048170   DQ048170 Homo sapi
     3   838.8   46.3   1056   3   BM925654   BM925654 AGENCOURT
     4   813.2   44.9   1322 14   DQ048171   DQ048171 Pan trogl
     5   783.4   43.2   1797 14   AY407808   AY407808 Homo sapi
     6   755.4   41.7   1797 14   AY407810   AY407810 Mus muscu
     7   732   40.4   879   2   BI756878   BI756878 603029069
     8   720.4   39.8   866 10   DV913368   DV913368 LB02827.C
     9   717.6   39.6   1120   3   BM907000   BM907000 AGENCOURT
    10   696   38.4   761   2   BI822362   BI822362 603037922
    11   676.6   37.3   806   8   CO886915   CO886915 BovGen_15
    12   675.6   37.3   839   5   CJ470325   CJ470325 CJ470325
    13   645   35.6   1016 10   DV011836   DV011836 CNB271-C0
    14   620.8   34.3   624   4   CB152086   CB152086 K-EST0209
    15   616.8   34.0   782   8   CN823582   CN823582 Oa_splbn_
    16   610.4   33.7   2031   6   AK048758   AK048758 Mus muscu
    17   604.8   33.4   652   5   CD630910   CD630910 56006229J
    18   602.4   33.2   1797 14   AY407809   AY407809 Pan trogl
    19   598.2   33.0   793   2   BI552481   BI552481 603196186
    20   593.8   32.8   1990   6   AK035817   AK035817 Mus muscu
    21   591   32.6   2617   6   AK051281   AK051281 Mus muscu
    22   588.4   32.5   596   9   DR001000   DR001000 TC112896
    23   588   32.5   588   9   DA406079   DA406079 DA406079
    24   582.4   32.1   596   9   DA586340   DA586340 DA586340
    25   580.4   32.0   1541   6   AK171529   AK171529 Mus muscu
    26   580   32.0   580   9   DA064328   DA064328 DA064328
    27   574.4   31.7   576   9   DA079387   DA079387 DA079387
    28   574   31.7   574   9   DA086071   DA086071 DA086071
    29   564   31.1   564   9   DA077079   DA077079 DA077079
    30   561   31.0   561   9   DA201413   DA201413 DA201413
    31   560.4   30.9   562   9   DA355587   DA355587 DA355587
    32   551.4   30.4   553   9   DA122336   DA122336 DA122336
    33   533.4   29.4   1578   6   AK170381   AK170381 Mus muscu
    34   526.2   29.0   531   4   CB154648   CB154648 K-EST0212
    35   522.6   28.8   1019   2   BM543465   BM543465 AGENCOURT
    36   519   28.6   555   9   DA074160   DA074160 DA074160
    37   519   28.6   825   3   BU458046   BU458046 603776544
    38   516.6   28.5   1046 10   DW666789   DW666789 CNB338-H1

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39   513.4   28.3   525    9   DA624069          DA624069 DA624069
40   512.8   28.3   517    4   CB153078          CB153078 K-EST0210
41   506.4   27.9   780    3   BU385765          BU385765 603861678
42   499.8   27.6   814    5   CJ430976          CJ430976 CJ430976
43   491.6   27.1   889   10   DV868862           DV868862 LB0251.CR
44   490.8   27.1  1048    9   DN684343          DN684343 CGX35-D06
45   486.2   26.8   990    3   BU273821          BU273821 603531731
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